SEOUENCE LISTING

SPERBER, ET AL. <110> INDUCTION OF APOPTOSIS BY HIV-1 INFECTED MONOCYTIC CELLS <120> 29636/38748 <130> <160> <170> PatentIn version 3.1 <210> 1 <211> 2279 <212> DNA <213> Homo sapiens <400> gctgacgggg tggcagtgcg gcgggttacg gcctggtcag accataatga cttcagcaaa 60 taaagcaatc gaattacaac tacaagtgaa acaaaatgca gaagaattac aagactttat 120 gcgggattta gaaaactggg aaaaagacat taaacaaaag gatatggaac taagaagaca 180 240 gaatggtgtt cctgaagaga atttacctcc tattcgaaat gggaatttta ggaaaaagaa 300 gaaaggcaaa gctaaagagt cttccaaaaa aaccagagag gaaaacacaa aaaacaggat aaaatettat gattatgagg catgggcaaa aettgatgtg gaeegtatee ttgatgaget 360 420 tgacaaagac gatagtaccc atgagtctct gtctcaagaa tcagagtcgg aagaagatgg 480 gattcatgta gattcacaaa aggctcttgt tttaaaagaa aagggcaata aatacttcaa 540 acaaggaaaa tatgatgaag caattgactg ctacacaaaa ggcatggatg ccgatccata 600 taatcccgtg ttgccaacga acagagcgtc agcatatttt agactgaaaa aatttgctgt tgctgagtct gattgtaatt tagcagttgc cttgaataga agttatacaa aggcttattc 660 720 cagacgaggt gctgctcgat ttgctttgca aaaattagaa gaggccaaaa aagattatga aagagtatta gaactagaac caaataactt tgaagcaaca aatgaactca ggaaaatcag 780 tcaggettta geatecaaag aaaaeteata tecaaaggaa getgacatag tgattaagte 840 900 aacagaagga gagcgaaagc aaattgaagc acaacagaat aagcagcagg ccatttcaga gaaagatcgg gggaatggat ttttcaaaga ggggaaatat gaaagagcaa ttgaatgcta 960 1020 tactcgaggg atagcagcag atggtgctaa tgcccttctt ccagctaaca gagctatggc 1080 ctatctgaag attcagaaat atgaagaagc tgaaaaagac tgcacacaag ccattttatt agatggctca tattctaaag cttttgccag aagaggaact gcaagaacat ttttgggaaa 1140 1200 gctaaatgag gcaaaacaag attttgaaac tgttttactt ctggaacctg gaaataagca 1260 agcagtaact gaactctcca aaattaaaaa ggaattaatt gagaaaggac actgggatga tgtctttctt gattccacac aaagacaaaa tgtggtaaaa cccattgata atccaccgca 1320

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Lys Asp Ile Lys Gln Lys Asp Met Glu Leu Arg Arg Gln Asn Gly Val $_{35}$ 40 45

Pro Glu Glu Asn Leu Pro Pro Ile Arg Asn Gly Asn Phe Arg Lys Lys 50 55 60

Lys Lys Gly Lys Ala Lys Glu Ser Ser Lys Lys Thr Arg Glu Glu Asn 65 70 75 80

Thr Lys Asn Arg Ile Lys Ser Tyr Asp Tyr Glu Ala Trp Ala Lys Leu 85 90 95 Asp Val Asp Arg Ile Leu Asp Glu Leu Asp Lys Asp Asp Ser Thr His 100 105 Glu Ser Leu Ser Gln Glu Ser Glu Ser Glu Glu Asp Gly Ile His Val 120 Asp Ser Gln Lys Ala Leu Val Leu Lys Glu Lys Gly Asn Lys Tyr Phe Lys Gln Gly Lys Tyr Asp Glu Ala Ile Asp Cys Tyr Thr Lys Gly Met 145 150 155 Asp Ala Asp Pro Tyr Asn Pro Val Leu Pro Thr Asn Arg Ala Ser Ala 165 Tyr Phe Arg Leu Lys Lys Phe Ala Val Ala Glu Ser Asp Cys Asn Leu 185 Ala Val Ala Leu Asn Arg Ser Tyr Thr Lys Ala Tyr Ser Arg Arg Gly 200 Ala Ala Arg Phe Ala Leu Gln Lys Leu Glu Glu Ala Lys Lys Asp Tyr 210 215 220 Glu Arg Val Leu Glu Leu Glu Pro Asn Asn Phe Glu Ala Thr Asn Glu 225 230 Leu Arg Lys Ile Ser Gln Ala Leu Ala Ser Lys Glu Asn Ser Tyr Pro 245 255 Lys Glu Ala Asp Ile Val Ile Lys Ser Thr Glu Gly Glu Arg Lys Gln Ile Glu Ala Gln Gln Asn Lys Gln Gln Ala Ile Ser Glu Lys Asp Arg Gly Asn Gly Phe Phe Lys Glu Gly Lys Tyr Glu Arg Ala Ile Glu Cys Tyr Thr Arg Gly Ile Ala Ala Asp Gly Ala Asn Ala Leu Leu Pro Ala 310 315 Asn Arg Ala Met Ala Tyr Leu Lys Ile Gln Lys Tyr Glu Glu Ala Glu 325 330 Lys Asp Cys Thr Gln Ala Ile Leu Leu Asp Gly Ser Tyr Ser Lys Ala

345

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- Ala Lys Gln Asp Phe Glu Thr Val Leu Leu Glu Pro Gly Asn Lys 370 375 380
- Gln Ala Val Thr Glu Leu Ser Lys Ile Lys Lys Glu Leu Ile Glu Lys 385 390 395 400
- Gly His Trp Asp Asp Val Phe Leu Asp Ser Thr Gln Arg Gln Asn Val 405 410 415
- Val Lys Pro Ile Asp Asn Pro Pro His Pro Gly Ser Thr Lys Pro Leu 420 425 430
- Lys Lys Val Ile Ile Glu Glu Thr Gly Asn Leu Ile Gln Thr Ile Asp 435 440 445
- Val Pro Asp Ser Thr Thr Ala Ala Pro Glu Asn Asn Pro Ile Asn 450 455 460
- Leu Ala Asn Val Ile Ala Ala Thr Gly Thr Thr Ser Lys Lys Asn Ser 465 470 475 480
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- Leu Lys Ile Glu Glu Val Ser Asp Thr Ser Ser Leu Gln Pro Gln Ala 500 505 510
- Ser Leu Lys Gln Asp Val Cys Gln Ser Tyr Ser Glu Lys Met Pro Ile 515 520 525
- Glu Ile Glu Gln Lys Pro Ala Gln Phe Ala Thr Thr Val Leu Pro Pro 530 535 540
- Ile Pro Ala Asn Ser Phe Gln Leu Glu Ser Asp Phe Arg Gln Leu Lys545550555560
- Ser Ser Pro Asp Met Leu Tyr Gln Tyr Leu Lys Gln Ile Glu Pro Ser 565 570 575
- Leu Tyr Pro Lys Leu Phe Gln Lys Asn Leu Asp Pro Asp Val Phe Asn 580 590
- Gln Ile Val Lys Ile Leu His Asp Phe Tyr Ile Glu Lys Glu Lys Pro 595 600 605

Leu Leu Ile Phe Glu Ile Leu Gln Arg Leu Ser Glu Leu Lys Arg Phe 615

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Leu Leu Glu Pro Gly Asn Lys Gln Ala Val Thr Glu Leu Ser Lys Ile

Lys Lys Glu Leu Ile Glu Lys Gly His Trp Asp Asp Val Phe Leu Asp

Ser Thr Gln Arg Gln Asn Val Val Lys Pro Ile Asp Asn Pro Pro His

Pro Gly Ser Thr Lys Pro Leu Lys Lys Val Ile Ile Glu Glu Thr Gly 105

Asn Leu Ile Gln Thr Ile Asp Val Pro Asp Ser Thr Thr Ala Ala Ala 115

Pro Glu Asn Asn Pro Ile Asn Leu Ala Asn Val Ile Ala Ala Thr Gly 130 135

Thr Thr Ser Lys Lys Asn Ser Ser Gln Asp Val Leu Phe Pro Thr Ser 150

Asp Thr Pro Arg Ala Lys Val Leu Lys Ile Glu Glu Val Ser Asp Thr 170 Ser Ser Leu Gln Pro Gln Ala Ser Leu Lys Gln Asp Val Cys Gln Ser 185 180 Tyr Ser Glu Lys Met Pro Ile Glu Ile Glu Gln Lys Pro Ala Gln Phe Ala Thr Thr Val Leu Pro Pro Ile Pro Ala Asn Ser Phe Gln Leu Glu Ser Asp Phe Arg Gln Leu Lys Ser Ser Pro Asp Met Leu Tyr Gln Tyr 235 230 Leu Lys Gln Ile Glu Pro Ser Leu Tyr Pro Lys Leu Phe Gln Lys Asn 250 Leu Asp Pro Asp Val Phe Asn Gln Ile Val Lys Ile Leu His Asp Phe 260 265 Tyr Ile Glu Lys Glu Lys Pro Leu Leu Ile Phe Glu Ile Leu Gln Arg 280 275 Leu Ser Glu Leu Lys Arg Phe Asp Met Ala Val Met Phe Met Ser Glu 290 295 300 Thr Glu Lys Lys Ile Ala Arg Ala Leu Phe Asn His Ile Asp Lys Ser 315 Gly Leu Lys Asp Ser Ser Val Glu Glu Leu Lys Lys 325 <210> 4 <211> 49 <213> Artificial sequence <220> <223> Linker-primer designed with a GAGA sequence to protect the Xho I restriction site and an 18-base (dT) sequence <400> 4 gagagagaga gagagagaaa ctagtctcga gtttttttt ttttttt 49 <210> 5 13 <211> <212> DNA

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	Artificial sequence
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